

SCORE Search Results Details for Application 10552515 and Search Result 20080624_135918_us-10-552-515-1_copy_157_933.szlm.rup.

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This page gives you Search Results detail for the Application 10552515 and Search Result 20080624_135918_us-10-552-515-1_copy_157_933.szlm.rup.

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OM protein - protein search, using sw model

Run on: June 24, 2008, 15:38:05 ; Search time 510 Seconds
(without alignments)
2506.345 Million cell updates/sec

Title: US-10-552-515-1_COPY_157_933
Perfect score: 4123
Sequence: 1 QQDVQDGNTTVHYALLSASW.....SELSSHWTPTVTPKASQLQQ 777

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5032670 seqs, 1645091341 residues

Total number of hits satisfying chosen parameters: 19795

Minimum DB seq length: 8
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_12.1:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	44	1.1	20	2 Q594K2_PLAFA	Q594k2 plasmodium
2	42	1.0	20	2 Q6BDK5_TRIMT	Q6bdk5 tricholoma
3	41	1.0	18	2 Q4XC48_PLACH	Q4xc48 plasmodium

4	39	0.9	17	2	Q76N52_HUMAN	Q76n52	homo sapien
5	39	0.9	17	2	Q5YKQ3_CONMU	Q5ykq3	conus mus (
6	39	0.9	18	1	CWP19_SOLLC	P80815	solanum lyc
7	39	0.9	18	2	Q62256_MOUSE	Q62256	mus musculu
8	39	0.9	19	2	A1Z5I9_HUMAN	A1z5i9	homo sapien
9	39	0.9	19	2	A2CIY7_RABIT	A2ciy7	oryctolagus
10	38.5	0.9	20	2	Q96RQ2_HUMAN	Q96rq2	homo sapien
11	38.5	0.9	20	2	Q4XES0_PLACH	Q4xes0	plasmodium
12	38	0.9	14	1	LPW_ECO57	P0ad94	escherichia
13	38	0.9	14	1	LPW_ECOL6	P0ad93	escherichia
14	38	0.9	14	1	LPW_ECOLI	P0ad92	escherichia
15	38	0.9	14	1	LPW_SHIFL	P0ad95	shigella fl
16	38	0.9	14	2	Q32GS5_SHIDS	Q32gs5	shigella dy
17	38	0.9	18	2	Q9LAP4_ENTFC	Q9lap4	enterococcu
18	38	0.9	19	2	Q3HYD3_TENMO	Q3hyd3	tenebrio mo
19	37.5	0.9	20	2	A6C5A0_9PLAN	A6c5a0	planctomyce
20	37	0.9	15	2	Q7M0C2_RAT	Q7m0c2	rattus norv
21	37	0.9	17	2	Q6PT69_LOLPR	Q6pt69	lolium pere
22	37	0.9	17	2	Q6PT67_9POAL	Q6pt67	streptochae
23	37	0.9	17	2	Q6PT68_SORBI	Q6pt68	sorghum bic
24	37	0.9	17	2	Q6PT72_9POAL	Q6pt72	bouteloua g
25	37	0.9	17	2	Q6PT71_9POAL	Q6pt71	chasmanthiu
26	37	0.9	17	2	Q6PT66_9ORYZ	Q6pt66	zizania aqu
27	37	0.9	17	2	Q6PT70_DANSP	Q6pt70	danthonia s
28	37	0.9	19	2	Q4Z5V1_PLABE	Q4z5v1	plasmodium
29	37	0.9	20	2	Q7JMY8_LEIIN	Q7jmy8	leishmania
30	37	0.9	20	2	Q7M4A5_MYTED	Q7m4a5	mytilus edu
31	37	0.9	20	2	Q9QW31_9MURI	Q9qw31	rattus sp.
32	37	0.9	20	2	Q7LZH3_MELGA	Q7lzh3	meleagris g
33	36	0.9	17	2	Q5YKQ8_CONGA	Q5ykq8	conus gladi
34	36	0.9	17	2	Q9QUJ4_9MURI	Q9quj4	mus sp. mep
35	36	0.9	19	2	Q9QV70_9MURI	Q9qv70	rattus sp.
36	36	0.9	20	1	2SS1_BRARC	P84529	brassica ra
37	36	0.9	20	1	PEP18_ARGAU	P84749	argiope aur
38	36	0.9	20	2	Q9S8B6_HORVU	Q9s8b6	hordeum vul
39	35.5	0.9	18	2	Q52RG5_HUMAN	Q52rg5	homo sapien
40	35.5	0.9	18	2	Q52RG4_HUMAN	Q52rg4	homo sapien
41	35.5	0.9	20	2	A5XL80_BURMA	A5xl80	burkholderi
42	35	0.8	15	2	Q5EDM6_LEGPN	Q5edm6	legionella
43	35	0.8	15	2	Q8UM88_9HIV1	Q8um88	human immun
44	35	0.8	16	1	ARCD_PSEPU	P41147	pseudomonas
45	35	0.8	19	2	Q06028_MOUSE	Q06028	mus musculu

ALIGNMENTS

RESULT 1

Q594K2_PLAFA

ID Q594K2_PLAFA Unreviewed; 20 AA.

AC Q594K2;

DT 26-APR-2005, integrated into UniProtKB/TrEMBL.

DT 26-APR-2005, sequence version 1.

DT 24-JUL-2007, entry version 7.

DE Digestive vacuole transmembrane protein (Fragment).

GN Name=CRT;

OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida;
 OC Plasmodium; Plasmodium (Laverania).
 OX NCBI_TaxID=5833;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GUY-PHG13;
 RA Best Plummer W., Pinto Pereira L.M., Carrington C.V.F.;
 RT "Pfcr1 and Pfmdr1 Alleles Associated with Chloroquine Resistance in
 RT Plasmodium falciparum from Guyana, South America."
 RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; AY570260; AAU03451.1; -; Genomic_DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA:UniProtKB-KW.
 PE 4: Predicted;
 KW Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2349 MW; 99A32D09DD195484 CRC64;

Query Match 1.1%; Score 44; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 3.8e+04;
 Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 399 VFILILSKIYVSLAHVLT 416
 :|| ||| ||:|:: ::|
 Db 1 IFIYILSIIYLSVSVMIT 18

RESULT 2

Q6BDK5_TRIMT

ID Q6BDK5_TRIMT Unreviewed; 20 AA.
 AC Q6BDK5;
 DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2004, sequence version 1.
 DT 24-JUL-2007, entry version 8.
 DE Putative uncharacterized protein (Fragment).
 OS Tricholoma matsutake (Matsutake mushroom) (Tricholoma nauseosum).
 OC Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;
 OC Agaricomycetes; Agaricomycetidae; Agaricales; Tricholomataceae;
 OC Tricholoma.
 OX NCBI_TaxID=40145;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Murata H.;
 RT "Characterization of the insertion sites of marY1, the gypsy-type
 RT retrotransposon from the ectomycorrhizal basidiomycete Tricholoma
 RT matsutake strain Y1, in the genome the fungus based on the inter-
 RT retrotransposon amplified polymorphism analysis."
 RL Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR  EMBL; AB160895; BAD32671.1; -; Genomic_DNA.
PE  4: Predicted;
FT  NON_TER      1      1
FT  NON_TER      20     20
SQ  SEQUENCE     20 AA;  2213 MW;  84BDB0AB47F6443C CRC64;

Query Match          1.0%;  Score 42;  DB 2;  Length 20;
Best Local Similarity 52.9%;  Pred. No. 5.6e+04;
Matches      9;  Conservative      1;  Mismatches      7;  Indels      0;  Gaps      0;

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Qy      618 HLAVISNAFLLAFFSSDF 634
      |:  ||  |  |||||
Db      1  HILGISKGILRVFSSDF 17

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RESULT 3

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Q4XC48_PLACH
ID  Q4XC48_PLACH          Unreviewed;          18 AA.
AC  Q4XC48;
DT  05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT  05-JUL-2005, sequence version 1.
DT  24-JUL-2007, entry version 7.
DE  Putative uncharacterized protein (Fragment).
GN  ORFNames=PC403567.00.0;
OS  Plasmodium chabaudi.
OC  Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida;
OC  Plasmodium; Plasmodium (Vincetia).
OX  NCBI_TaxID=5825;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  PubMed=15637271; DOI=10.1126/science.1103717;
RA  Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA  Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA  James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA  Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA  Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA  Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA  Sinden R.S.;
RT  "A comprehensive survey of the Plasmodium life cycle by genomic,
RT  transcriptomic, and proteomic analyses.";
RL  Science 307:82-86(2005).
CC  -!- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
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CC -----
DR  EMBL; CAAJ01007713; CAH85524.1; -; Genomic_DNA.
PE  4: Predicted;
FT  NON_TER      1      1
SQ  SEQUENCE     18 AA;  2011 MW;  674A05D1A9721915 CRC64;

Query Match          1.0%;  Score 41;  DB 2;  Length 18;
Best Local Similarity 50.0%;  Pred. No. 5.9e+04;

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Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 607 GIWFHILAGL 616
|:| | |:| |
Db 7 GVWFFVLSGI 16

RESULT 4

Q76N52_HUMAN

ID Q76N52_HUMAN Unreviewed; 17 AA.
AC Q76N52;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 24-JUL-2007, entry version 12.
DE Ribosomal protein L41 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98248690; PubMed=9582194;
RA Kenmochi N., Kawaguchi T., Rozen S., Davis E., Goodman N.,
RA Hudson T.J., Tanaka T., Page D.C.;
RT "A map of 75 human ribosomal protein genes."
RL Genome Res. 8:509-523(1998).
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CC -----
DR EMBL; AB007186; BAA28285.1; -; Genomic_DNA.
DR UniGene; Hs.112553; -.
DR UniGene; Hs.242947; -.
DR UniGene; Hs.282998; -.
DR UniGene; Hs.356799; -.
DR UniGene; Hs.434890; -.
DR UniGene; Hs.532082; -.
DR UniGene; Hs.632703; -.
DR UniGene; Hs.649959; -.
DR HGNC; HGNC:10354; RPL41.
PE 4: Predicted;
KW Ribosomal protein.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 2385 MW; 1990EBE3EEA7E344 CRC64;

Query Match 0.9%; Score 39; DB 2; Length 17;
Best Local Similarity 43.8%; Pred. No. 8.1e+04;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 509 LKGWWQKFRLRSKRRK 524
:: |:| |:| |||
Db 1 MRAKWRKKRMRRLKRRK 16

RESULT 5

Q5YKQ3_CONMU

ID Q5YKQ3_CONMU Unreviewed; 17 AA.
AC Q5YKQ3;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 24-JUL-2007, entry version 8.
DE Calmodulin (Fragment).
OS Conus mus (Mouse cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=257335;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Duda T.F. Jr.;
RT "Divergence in tropical seas: Global biogeography and evolutionary
RT history of the marine gastropod genus Conus."
RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; AY382052; AAS01366.1; -; Genomic_DNA.
DR GO; GO:0005509; F:calcium ion binding; IEA:InterPro.
DR InterPro; IPR002048; EF_hand_Ca_bd.
DR PROSITE; PS50222; EF_HAND_2; 1.
PE 4: Predicted;
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1835 MW; B6BEFE6AD2DD90F6 CRC64;

Query Match 0.9%; Score 39; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 8.1e+04;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 DGNTTVHYA 14
||| |:|:|
Db 5 DGNGTIHFA 13

RESULT 6

CWP19_SOLLC

ID CWP19_SOLLC Reviewed; 18 AA.
AC P80815;
DT 25-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 25-OCT-2005, sequence version 1.
DT 24-JUL-2007, entry version 9.
DE 76 kDa cell wall protein (Fragment).
OS Solanum lycopersicum (Tomato) (Lycopersicon esculentum).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiids; Solanales; Solanaceae; Solanoideae; Solaneae;
OC Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
RN [1]
RP PROTEIN SEQUENCE, AND SUBCELLULAR LOCATION.

RX MEDLINE=97332671; PubMed=9188482; DOI=10.1074/jbc.272.25.15841;
 RA Robertson D., Mitchell G.P., Gilroy J.S., Gerrish C., Bolwell G.P.,
 RA Slabas A.R.;
 RT "Differential extraction and protein sequencing reveals major
 RT differences in patterns of primary cell wall proteins from plants."
 RL J. Biol. Chem. 272:15841-15848(1997).
 CC -!- SUBCELLULAR LOCATION: Secreted, cell wall.
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 PE 1: Evidence at protein level;
 KW Cell wall; Direct protein sequencing; Secreted.
 FT CHAIN 1 >18 76 kDa cell wall protein.
 FT /FTId=PRO_0000079688.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1994 MW; 26676172F5F28409 CRC64;

 Query Match 0.9%; Score 39; DB 1; Length 18;
 Best Local Similarity 63.6%; Pred. No. 8.7e+04;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 80 KLPRFLGSDNQ 90
 : | ||| |||
 Db 3 RTPEFLGLDNQ 13

RESULT 7

Q62256_MOUSE

ID Q62256_MOUSE Unreviewed; 18 AA.
 AC Q62256;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1996, sequence version 1.
 DT 24-JUL-2007, entry version 20.
 DE Spermatogenic-specific proenkephalin.
 GN Name=Penk-rs;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=90287163; PubMed=2355920;
 RA Kilpatrick D.L., Zinn S.A., Fitzgerald M., Higuchi H., Sabol S.L.,
 RA Meyerhardt J.;
 RT "Transcription of the rat and mouse proenkephalin genes is initiated
 RT at distinct sites in spermatogenic and somatic cells."
 RL Mol. Cell. Biol. 10:3717-3726(1990).
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 CC -----
 DR EMBL; M55181; AAA40127.1; -; mRNA.
 DR PIR; A35678; A35678.
 DR MGI; MGI:104628; Penk-rs.

PE 4: Predicted;
SQ SEQUENCE 18 AA; 2043 MW; B96E10CC7049FA76 CRC64;

Query Match 0.9%; Score 39; DB 2; Length 18;
Best Local Similarity 54.5%; Pred. No. 8.7e+04;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 528 SAGASQGPWED 538
|:| |||
Db 2 SSGKQDSPWED 12

RESULT 8
A1Z5I9_HUMAN
ID A1Z5I9_HUMAN Unreviewed; 19 AA.
AC A1Z5I9;
DT 06-FEB-2007, integrated into UniProtKB/TrEMBL.
DT 06-FEB-2007, sequence version 1.
DT 24-JUL-2007, entry version 2.
DE Mediator of DNA damage checkpoint 1 variant 1 (Fragment).
GN Name=MDC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bu Y., Ozaki T., Suenaga Y., Nakanishi M., Kamijo T., Song F.,
RA Nakagawara A.;
RT "Identification and characterization of human NFBD1 promoter.";
RL Submitted (DEC-2006) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; EF177823; ABM47421.1; -; mRNA.
PE 4: Predicted;
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2326 MW; 0200C23525665A0E CRC64;

Query Match 0.9%; Score 39; DB 2; Length 19;
Best Local Similarity 43.8%; Pred. No. 9.3e+04;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 291 TLAYRWDCSDYEDTEE 306
| | || : |:|:
Db 4 TQAIDWDVEEEEETE Q 19

RESULT 9
A2CIY7_RABIT
ID A2CIY7_RABIT Unreviewed; 19 AA.
AC A2CIY7;
DT 20-FEB-2007, integrated into UniProtKB/TrEMBL.
DT 20-FEB-2007, sequence version 1.

DT 24-JUL-2007, entry version 3.
DE O-mannosyl N-acetylglucosaminyltransferase (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=17345675;
RA Farwick A., Jordan U., Fuellen G., Huchon D., Catzeflis F.,
RA Brosius J., Schmitz J.;
RT "Automated scanning for phylogenetically informative transposed
RT elements in rodents.";
RL Syst. Biol. 55:936-948(2006).
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CC -----
DR EMBL; DQ451084; ABE41717.1; -; Genomic_DNA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA:UniProtKB-KW.
PE 4: Predicted;
KW Glycosyltransferase; Transferase.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2202 MW; D7445A61F812B998 CRC64;

Query Match 0.9%; Score 39; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 9.3e+04;
Matches 7; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 167 WGKWN--KYQPLDH 178
|| || : : |||
Db 3 WGTWNVDEAEVL DH 16

RESULT 10

Q96RQ2_HUMAN

ID Q96RQ2_HUMAN Unreviewed; 20 AA.
AC Q96RQ2;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 24-JUL-2007, entry version 13.
DE Natural killer cell receptor 2B4 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21240684; PubMed=11342640;
RA Chuang S.S., Pham H.T., Kumaresan P.R., Mathew P.A.;
RT "A prominent role for activator protein-1 in the transcription of the
RT human 2B4 (CD244) gene in NK cells.";
RL J. Immunol. 166:6188-6195(2001).

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CC -----
DR EMBL; AF297616; AAK57926.1; -; Genomic_DNA.
DR UniGene; Hs.157872; -.
DR HGNC; HGNC:18171; CD244.
DR GO; GO:0004872; F:receptor activity; IEA:UniProtKB-KW.
PE 4: Predicted;
KW Receptor.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2243 MW; EBF997A9C0CF71EB CRC64;

Query Match 0.9%; Score 38.5; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 1.1e+05;
Matches 8; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Qy 391 LTGSVVNLVFILILSKIY 408
: | || |: |:| |:|
Db 1 MLGQVVTLILLLLL-KVY 17

RESULT 11

Q4XES0_PLACH

ID Q4XES0_PLACH Unreviewed; 20 AA.
AC Q4XES0;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 24-JUL-2007, entry version 7.
DE Putative uncharacterized protein (Fragment).
GN ORFNames=PC402444.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida;
OC Plasmodium; Plasmodium (Vinckeia).
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; CAAJ01006918; CAH84598.1; -; Genomic_DNA.

PE 4: Predicted;
FT NON_TER 1 1
SQ SEQUENCE 20 AA; 2329 MW; FA3AE53FC706E353 CRC64;

Query Match 0.9%; Score 38.5; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy 432 TLKVFIFQFVNFYSSPVYIA 451
| | |||:| | : |: ||
Db 1 TQKGFIFKF-NMFGPLPLKIA 19

RESULT 12

LPW_ECO57

ID LPW_ECO57 Reviewed; 14 AA.
AC P0AD94; P03053;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 24-JUL-2007, entry version 11.
DE Trp operon leader peptide.
GN Name=trpL; OrderedLocusNames=Z2545, ECs1837;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796; DOI=10.1093/dnares/8.1.11;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -!- FUNCTION: This protein is involved in control of the biosynthesis
CC of tryptophan (By similarity).
CC -----
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CC -----
DR EMBL; AE005174; AAG56550.1; -; Genomic_DNA.

DR EMBL; BA000007; BAB35260.1; -; Genomic_DNA.
DR PIR; B85761; B85761.
DR PIR; E90858; E90858.
DR GenomeReviews; BA000007_GR; ECs1837.
DR GenomeReviews; AE005174_GR; Z2545.
DR KEGG; ece:Z2545; -.
DR KEGG; ecs:ECs1837; -.
DR InterPro; IPR013205; Leader_Trp_op.
DR Pfam; PF08255; Leader_Trp; 1.
PE 3: Inferred from homology;
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW Complete proteome; Leader peptide; Tryptophan biosynthesis.
FT PEPTIDE 1 14 Trp operon leader peptide.
FT /FTId=PRO_0000044024.
SQ SEQUENCE 14 AA; 1723 MW; 5B79306E3E804A37 CRC64;

Query Match 0.9%; Score 38; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 7.6e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 509 LKGWWQ 514
|||||:
Db 7 LKGWWR 12

RESULT 13

LPW_ECOL6

ID LPW_ECOL6 Reviewed; 14 AA.
AC P0AD93; P03053;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 21-AUG-2007, entry version 13.
DE Trp operon leader peptide.
GN Name=trpL; OrderedLocusNames=c5494;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC -!- FUNCTION: This protein is involved in control of the biosynthesis
CC of tryptophan (By similarity).
CC -----
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CC -----
DR EMBL; AE014075; AAN80196.1; -; Genomic_DNA.

DR GenomeReviews; AE014075_GR; c_5494.
 DR KEGG; ecc:c5494; -.
 DR InterPro; IPR013205; Leader_Trp_op.
 DR Pfam; PF08255; Leader_Trp; 1.
 PE 3: Inferred from homology;
 KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
 KW Complete proteome; Leader peptide; Tryptophan biosynthesis.
 FT PEPTIDE 1 14 Trp operon leader peptide.
 FT /FTId=PRO_0000044025.
 SQ SEQUENCE 14 AA; 1723 MW; 5B79306E3E804A37 CRC64;

Query Match 0.9%; Score 38; DB 1; Length 14;
 Best Local Similarity 83.3%; Pred. No. 7.6e+04;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 509 LKGWWQ 514
 |||||:
 Db 7 LKGWWR 12

RESULT 14

LPW_ECOLI

ID LPW_ECOLI Reviewed; 14 AA.
 AC P0AD92; P03053; Q2MBG1;
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
 DT 21-JUL-1986, sequence version 1.
 DT 24-JUL-2007, entry version 14.
 DE Trp operon leader peptide.
 GN Name=trpL; Synonyms=trpEE; OrderedLocusNames=b1265, JW1257;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=82150258; PubMed=7038627; DOI=10.1093/nar/9.24.6647;
 RA Yanofsky C., Platt T., Crawford I.P., Nichols B.P., Christie G.E.,
 RA Horowitz H., van Cleemput M., Wu A.M.;
 RT "The complete nucleotide sequence of the tryptophan operon of
 RT Escherichia coli.";
 RL Nucleic Acids Res. 9:6647-6668(1981).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=76240562; PubMed=781271; DOI=10.1016/0022-2836(76)90317-X;
 RA Squires C., Lee F., Bertrand K., Squires C.L., Bronson M.J.,
 RA Yanofsky C.;
 RT "Nucleotide sequence of the 5' end of tryptophan messenger RNA of
 RT Escherichia coli.";
 RL J. Mol. Biol. 103:351-381(1976).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=80101455; PubMed=118451;
 RA Oxender D.L., Zurawski G., Yanofsky C.;
 RT "Attenuation in the Escherichia coli tryptophan operon: role of RNA
 RT secondary structure involving the tryptophan codon region.";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:5524-5528(1979).

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RN      [4]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=K12 / MG1655 / ATCC 47076;
RX      MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA      Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA      Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA      Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA      Mau B., Shao Y.;
RT      "The complete genome sequence of Escherichia coli K-12.";
RL      Science 277:1453-1474(1997).
RN      [5]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=K12 / W3110 / ATCC 27325 / DSM 5911;
RX      PubMed=16738553; DOI=10.1038/msb4100049;
RA      Hayashi K., Morooka N., Yamamoto Y., Fujita K., Isono K., Choi S.,
RA      Ohtsubo E., Baba T., Wanner B.L., Mori H., Horiuchi T.;
RT      "Highly accurate genome sequences of Escherichia coli K-12 strains
RT      MG1655 and W3110.";
RL      Mol. Syst. Biol. 2:E1-E5(2006).
RN      [6]
RP      STRUCTURE BY NMR.
RX      MEDLINE=94089403; PubMed=7505428; DOI=10.1093/nar/21.23.5485;
RA      Ramesh V.;
RT      "NMR evidence for the RNA stem-loop structure involved in the
RT      transcription attenuation of E. coli trp operon.";
RL      Nucleic Acids Res. 21:5485-5488(1993).
CC      -!- FUNCTION: This protein is involved in control of the biosynthesis
CC      of tryptophan.
CC      -----
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CC      -----
DR      EMBL; J01714; AAA57296.1; -; Genomic_DNA.
DR      EMBL; U00096; AAC74347.1; -; Genomic_DNA.
DR      EMBL; AP009048; BAE76395.1; -; Genomic_DNA.
DR      PIR; A03589; LFECW.
DR      GenomeReviews; U00096_GR; b1265.
DR      GenomeReviews; AP009048_GR; JW1257.
DR      KEGG; ecj:JW1257; -.
DR      KEGG; eco:b1265; -.
DR      EchoBASE; EB1252; -.
DR      EcoGene; EG11274; trpL.
DR      BioCyc; EcoCyc:EG11274-MONOMER; -.
DR      InterPro; IPR013205; Leader_Trp_op.
DR      Pfam; PF08255; Leader_Trp; 1.
PE      1: Evidence at protein level;
KW      Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW      Complete proteome; Leader peptide; Tryptophan biosynthesis.
FT      PEPTIDE           1           14           Trp operon leader peptide.
FT                                     /FTId=PRO_0000044023.
SQ      SEQUENCE      14 AA;  1723 MW;  5B79306E3E804A37 CRC64;

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Query Match 0.9%; Score 38; DB 1; Length 14;
 Best Local Similarity 83.3%; Pred. No. 7.6e+04;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 509 LKGWWQ 514
 |||||:
 Db 7 LKGWWR 12

RESULT 15

LPW_SHIFL

ID LPW_SHIFL Reviewed; 14 AA.
 AC P0AD95; P03053;
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
 DT 21-JUL-1986, sequence version 1.
 DT 21-AUG-2007, entry version 15.
 DE Trp operon leader peptide.
 GN Name=trpL; OrderedLocusNames=SF1268, S4805;
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=301 / Serotype 2a;
 RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RT through comparison with genomes of Escherichia coli K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 700930 / 2457T / Serotype 2a;
 RX MEDLINE=22590274; PubMed=12704152;
 RX DOI=10.1128/IAI.71.5.2775-2786.2003;
 RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
 RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
 RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
 RA Schwartz D.C., Blattner F.R.;
 RT "Complete genome sequence and comparative genomics of Shigella
 RT flexneri serotype 2a strain 2457T.";
 RL Infect. Immun. 71:2775-2786(2003).
 CC -!- FUNCTION: This protein is involved in control of the biosynthesis
 CC of tryptophan (By similarity).
 CC -----
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 CC -----
 DR EMBL; AE005674; AAN42881.1; -; Genomic_DNA.
 DR EMBL; AE014073; AAP16766.1; -; Genomic_DNA.
 DR GenomeReviews; AE014073_GR; S_4805.
 DR GenomeReviews; AE005674_GR; SF1268.
 DR KEGG; sfl:SF1268; -.
 DR KEGG; sfx:S4805; -.
 DR InterPro; IPR013205; Leader_Trp_op.
 DR Pfam; PF08255; Leader_Trp; 1.

PE 3: Inferred from homology;
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW Complete proteome; Leader peptide; Tryptophan biosynthesis.
FT PEPTIDE 1 14 Trp operon leader peptide.
FT /FTId=PRO_0000044029.
SQ SEQUENCE 14 AA; 1723 MW; 5B79306E3E804A37 CRC64;

Query Match 0.9%; Score 38; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 7.6e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 509 LKGWWQ 514
| | | | :
Db 7 LKGWWR 12

Search completed: June 24, 2008, 15:46:46
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SCORE 1.0